

VIA FIRST CLASS MAIL

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 By By *Norman D. Hanson*
 FULBRIGHT & JAWORSKI L.L.P.



GP 1642
 Box Seq 10
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 DEC 18 2000
 110161

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) : JAGER, et al.

TECH CENTER 1600/2900

Serial No. : 09/451,739

Filed : November 30, 1999

For : ISOLATED NUCLEIC ACID MOLECULES ENCODING
CANCER ASSOCIATED ANTIGENS, THE ANTIGENS
PER SE, AND USES THEREOF

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Group Art Unit : 1642

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Examiner : G. Nickol

TECH CENTER 1600/2900

December 8, 2000

Hon. Commissioner of Patents
and Trademarks
Washington, D.C. 20231

**LETTER RE
SEQUENCES**

Responsive to the office action of December 1, 2000, a copy of which is attached, please replace the paper copy of sequence information in this case and the computer readable form thereof with the attached. The undersigned hereby declares that, to the best of his knowledge, the information on the submitted paper copy is identical to the information in the computer readable form of sequence information, and both are identical to information presented in the application as filed. No new matter is believed to be presented.

Respectfully submitted,

FULBRIGHT & JAWORSKI L.P.By *Norman D. Hanson*

Norman D. Hanson
Reg. No. 30,946

666 Fifth Avenue
New York, New York 10103
(212) 318-3000

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TECH CENTER 1600

<110> Jager, Dirk
Scanlan, Matthew
Gure, Ali
Jager, Elke
Knuth, Alexander
Old, Lloyd
Chen, Yao-tseng



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X
S

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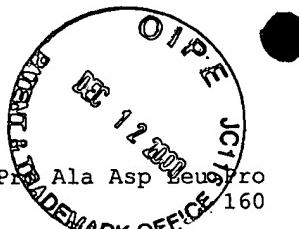
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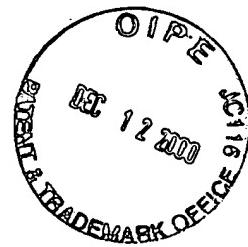
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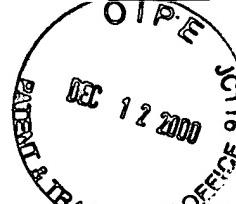
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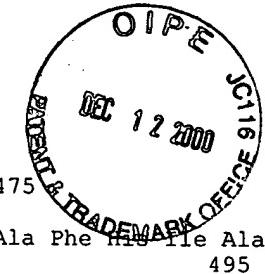
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470

475

480

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<212> PRT
<213> Homo sapiens
<400> 19
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1 5 10 15

Asp Pro Gly Pro Val Ala Arg Gly Arg Gly Cys Ser Ser Asp Arg Leu
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Pro Arg Pro Ala Gly Pro Ala Arg Arg Gln Phe Gln Ala Ala Ser Leu
35 40 45

Leu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Leu Lys
50 55 60

Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala
65 70 75 80

Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser
85 90 95

Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu
100 105 110

Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe
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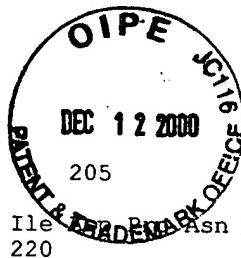
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130 135 140

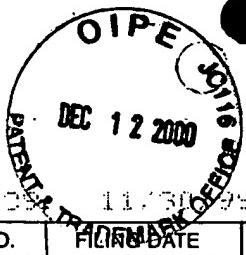
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Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn
165 170 175

Ala Ser Ser Asn His Asp His Asp Gly Ala Ser Gly Thr Pro Lys
180 185 190

Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Arg Ser Lys Ala Lys



**UNITED STATES DEPARTMENT OF COMMERCE****Patent and Trademark Office**Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

LUD-5615

APPLICATION NO.	FILED DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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024972
FULBRIGHT & JAWORSKI, LLP
656 FIFTH AVE
NEW YORK NY 10103-2196

HM12/1201

NICKOL, G

EXAMINER

1632

ART UNIT	PAPER NUMBER
----------	--------------

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

FULBRIGHT & JAWORSKI, LLP
NEW YORK DOCKETING

Docketed Not Required
Previously Updated

Docket No: LUD 5615-11741

Action: Sequence listing

Reminder: 12-25-2001

Date: Due/Done 12-25-2001

Initials:



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/451739			

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EXAMINER

ART UNIT PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

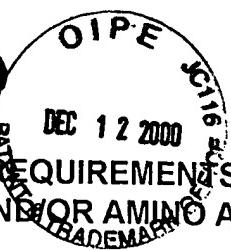
This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

Any inquiry concerning this communication should be directed to Examiner Gary Nickol, Ph.D., Art Unit 1642, whose telephone number is 703-305-7143.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

APPLICANT IS GIVEN A ONE MONTH EXTENDABLE PERIOD WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Susan L. Nickol
SUSAN L. NICKOL, PH.D.
PRIMARY EXAMINER



Application No. 09/451739

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing".
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: _____

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Applicant Must Provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

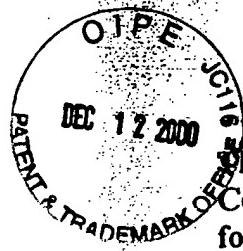
Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/451,739A

Source: 1642

Date Processed by STIC: 2/12/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

1642



G. Nickol

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/451,739A

DATE: 07/12/2000
TIME: 15:56:26

Input Set : A:\lud-5615.txt
Output Set: N:\CRF3\07122000\I451739A.raw

1 <110> APPLICANT: Jager, Dirk
2 Scanlan, Matthew
3 Gure, Ali
4 Jager, Elke
5 Knuth, Alexander
6 Old, Lloyd
7 Chen, Yao-tseng
9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
10 the Antigens per se, and Uses Thereof
12 <130> FILE REFERENCE: LUD 5615
14 <140> CURRENT APPLICATION NUMBER: 09/451,739A
16 <141> CURRENT FILING DATE: 1999-11-30
18 <160> NUMBER OF SEQ ID NOS: 19

ERRORED SEQUENCES

527 <210> SEQ ID NO: 16
528 <211> LENGTH: 528
529 <212> TYPE: PRT
530 <213> ORGANISM: Homo sapiens
531 <220> FEATURE:
532 <400> SEQUENCE: 16
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534 1 5 10 15
535 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
536 20 25 30
537 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
538 35 40 45
539 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
540 50 55 60
541 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
542 65 70 75 80
543 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
544 85 90 95
545 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
546 100 105 110
547 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
548 115 120 125
549 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
550 130 135 140
551 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
552 145 150 155 160
553 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
554 165 170 175
555 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
556 180 185 190

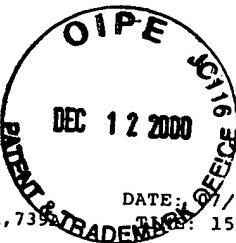
Does Not Comply
Corrected Diskette Needed

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REC'D BY FAX

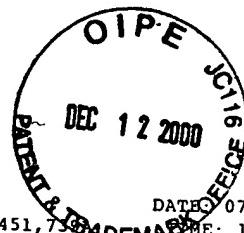
RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/451,739A

Input Set : A:\lud-5615.txt
Output Set: N:\CRF3\07122000\I451739A.raw

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572	Lys	Ala	Thr	His	Gln	Lys	Glu	Met	Asp	Lys	Ile	Ser	Gly	Lys	Leu	Glu
573	210							215						220		
575	Asp	Ser	Thr	Ser	Leu	Ser	Lys	Ile	Leu	Asp	Thr	Val	His	Ser	Cys	Glu
576	225						230						235			240
578	Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys
E-->	579	260	245					265	250				270	255		
581	Met	Glu	Gln	Met	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	Ser	
E-->	582	275	260					280	265				285	275		
584	Glu	Ala	Lys	Glu	Ile	Lys	Ser	Gin	Leu	Glu	Asn	Gln	Lys	Val	Lys	Trp
E-->	585	290	277					295	283				300	285		
587	Glu	Gln	Glu	Leu	Cys	Ser	Val	Arg	Leu	Thr	Leu	Asn	Gln	Glu	Glu	
E-->	588	305					310					315			320	
590	Lys	Arg	Arg	Asn	Ala	Asp	Ile	Leu	Asn	Glu	Ile	Arg	Glu	Glu		
E-->	591						325					330			335	
593	Gly	Arg	Ile	Glu	Clu	Gln	His	Arg	Lys	Glu	Leu	Glu	Val	Lys	Gln	
E-->	594						340					345			350	
596	Leu	Glu	Gln	Ala	Leu	Arg	Ile	Gln	Asp	Ile	Glu	Leu	Lys	Ser	Val	Glu
E-->	597						355					360			365	
599	Ser	Asn	Leu	Asn	Gln	Val	Ser	His	Thr	His	Glu	Asn	Glu	Asn	Tyr	Leu
E-->	600						370					375			380	
602	Leu	His	Glu	Asn	Cys	Met	Leu	Lys	Lys	Glu	Ile	Ala	Met	Leu	Lys	Leu
E-->	603	385					390					395			400	
605	Glu	Ile	Ala	Thr	Leu	Lys	His	Gln	Tyr	Gln	Glu	Lys	Glu	Asn	Lys	Tyr
E-->	606						405					410			415	
608	Phe	Glu	Asp	Ile	Lys	Ile	Leu	Lys	Glu	Lys	Asn	Ala	Glu	Leu	Gln	Met
E-->	609						420					425			430	
611	Thr	Leu	Lys	Leu	Lys	Glu	Ser	Leu	Thr	Lys	Arg	Ala	Ser	Gln	Tyr	
E-->	612						435					440			445	
614	Ser	Gly	Gln	Leu	Lys	Val	Leu	Ile	Ala	Glu	Asn	Thr	Met	Leu	Thr	Ser
E-->	615						450					455			460	
617	Lys	Leu	Lys	Glu	Lys	Gln	Asp	Lys	Glu	Ile	Leu	Glu	Ala	Glu	Ile	Glu
E-->	618	465					470					475			480	
620	Ser	His	His	Pro	Arg	Leu	Ala	Ser	Ala	Val	Gln	Asp	His	Asp	Gln	Ile
E-->	621						485					490			495	
623	Val	Thr	Ser	Arg	Lys	Ser	Gln	Glu	Pro	Ala	Phe	His	Ile	Ala	Gly	Asp
E-->	624						500					505			510	
626	Ala	Cys	Leu	Gln	Arg	Lys	Met	Asn	Val	Asp	Val	Ser	Ser	Thr	Asp	Ile
E-->	627						515					520			525	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/451,739 DATE: 07/12/2000

TIME: 15:56:27

Input Set : A:\lud-5615.txt

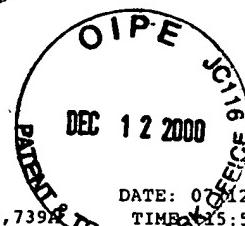
Output Set: N:\CRF3\07122000\I451739A.raw

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 L:28 M:283 W: Missing Blank Line separator, <400> field identifier
 L:35 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
 L:35 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
 L:86 M:283 W: Missing Blank Line separator, <220> field identifier
 L:87 M:283 W: Missing Blank Line separator, <220> field identifier
 L:133 M:283 W: Missing Blank Line separator, <400> field identifier
 L:134 M:283 W: Missing Blank Line separator, <220> field identifier
 L:166 M:283 W: Missing Blank Line separator, <400> field identifier
 L:167 M:283 W: Missing Blank Line separator, <220> field identifier
 L:203 M:283 W: Missing Blank Line separator, <220> field identifier
 L:204 M:283 W: Missing Blank Line separator, <400> field identifier
 L:264 M:283 W: Missing Blank Line separator, <220> field identifier
 L:265 M:283 W: Missing Blank Line separator, <400> field identifier
 L:313 M:283 W: Missing Blank Line separator, <220> field identifier
 L:314 M:283 W: Missing Blank Line separator, <400> field identifier
 L:365 M:283 W: Missing Blank Line separator, <220> field identifier
 L:368 M:283 W: Missing Blank Line separator, <400> field identifier
 L:391 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
 L:391 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
 L:400 M:283 W: Missing Blank Line separator, <220> field identifier
 L:401 M:283 W: Missing Blank Line separator, <400> field identifier
 L:409 M:283 W: Missing Blank Line separator, <220> field identifier
 L:410 M:283 W: Missing Blank Line separator, <400> field identifier
 L:418 M:283 W: Missing Blank Line separator, <220> field identifier
 L:419 M:283 W: Missing Blank Line separator, <400> field identifier
 L:427 M:283 W: Missing Blank Line separator, <220> field identifier
 L:428 M:283 W: Missing Blank Line separator, <400> field identifier
 L:436 M:283 W: Missing Blank Line separator, <220> field identifier
 L:437 M:283 W: Missing Blank Line separator, <400> field identifier
 L:445 M:283 W: Missing Blank Line separator, <220> field identifier
 L:446 M:283 W: Missing Blank Line separator, <400> field identifier
 L:454 M:283 W: Missing Blank Line separator, <220> field identifier
 L:457 M:283 W: Missing Blank Line separator, <400> field identifier
 L:512 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:512 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
 L:516 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
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 L:522 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:522 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
 L:524 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
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 L:532 M:283 W: Missing Blank Line separator, <400> field identifier
 L:579 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:582 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/451,739A

DATE: 07/12/2000
TIME: 15:56:27Input Set : A:\lud-5615.txt
Output Set: N:\CRF3\07122000\I451739A.raw

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 L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:594 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:597 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:600 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:603 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:606 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:612 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:615 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:618 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:621 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:624 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:627 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:627 M:252 E: No. of Seq. differs, <211>LENGTH:Input:528 Found:512 SEQ:16
 L:631 M:283 W: Missing Blank Line separator, <220> field identifier
 L:635 M:283 W: Missing Blank Line separator, <400> field identifier
 L:643 M:283 W: Missing Blank Line separator, <220> field identifier
 L:644 M:283 W: Missing Blank Line separator, <400> field identifier
 L:652 M:283 W: Missing Blank Line separator, <220> field identifier
 L:653 M:283 W: Missing Blank Line separator, <400> field identifier

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